REMARKS

Entry of the amendments and examination in view of the amendments is respectfully requested. Based on the amendments and the accompanying discussion it is submitted that the claims as amended describe patentable subject matter, and therefore it is requested that the examiner consider the application in view of the amendments.

I. The Amendments

Many of the amendments are grammatical or serve to more particularly define the invention, and do not add new matter. The amendment to be inserted at page 1, line 7, sets forth the relationship of the present application to related applications. The amendment to be inserted at page 12, line 13 simply copies into the specification the text of claims 15 and 16 as originally filed, and as such adds no new matter.

The amendments to the Sequence Listing are to make the Sequence Listing consistent with the current requirements for form. No new matter is added.

Support for claim 14 as amended is found at least at page 12, line 34 to page 13, line 9; page 17, line 28 to page 18, line 8; page 37, line 4 to page 38, line 3; page 40, line 13 to page 42, line 32; page 54, line 25 to page 55, line 1 and Figures 1 and 2.

Support for claim 15 as amended is found at least at page 37, line 29 to page 38, line 3.

Support for claim 16 as amended is found at least at page 37, line 29 to page 38, line 3. page 40, line 13 to page 42, line 32; and Figure 2.

Support for claim 17 as amended is found at least at page 12, line 34 to page 13, line 9; page 17, line 28 to page 18, line 8; page 37, line 4 to page 38, line 3; page 40, line 13 to page 42, line 32; page 54, line 25 to page 55, line 1 and Figures 1 and 2.

As can be seen from the support identified above, no new matter is added by the amendments.

II. Summary

Entry of the amendments is respectfully requested. The Examiner is invited to telephone the undersigned if it would be considered helpful in examining the application.

Respectfully submitted,

Dated: 9/25/01

By ______________________
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APPENDIX A

MARKED-UP VERSION OF AMENDMENTS TO THE SPECIFICATION

At page 7, line 28, please amend the specification as follows:

It is unlikely that all mRNAs are amenable to detection by this method for the following reasons. For an mRNA to surface in such a survey, it must be prevalent enough to produce a signal on the autoradiograph and contain a sequence in its 3′ 500 nucleotides capable of serving as a site for mismatched primer binding and priming. The more prevalent an individual mRNA species, the more likely it would be to generate a product. Thus, prevalent species may give bands with many different arbitrary primers. Because this latter property would contain an unpredictable element of chance based on selection of the arbitrary primers, it would be difficult to approach closure by the arbitrary primer method. Also, for the information to be portable from one laboratory to another and reliable, the mismatched priming must be highly reproducible under different laboratory conditions using different PCR machines, with [he]the resulting slight variation in reaction conditions. As the basis for mismatched priming is poorly understood, this is a drawback of building a database from data obtained by the Liang & Pardee differential display method.

APPENDIX B

MARKED-UP VERSION OF AMENDMENT TO CLAIMS 14-17

14. [The method of claim 1 wherein the step of generating linearized fragments of the cloned inserts comprises:

(i) dividing the plasmid containing the insert into two fractions, a first fraction cleaved with the restriction endonuclease XhoI and a second fraction cleaved with the restriction endonuclease SalI;

(ii) recombining the first and second fractions after cleavage;

(iii) dividing the recombined fractions into thirds and cleaving the first third with the restriction endonuclease HindIII, the second third with the restriction endonuclease BamHI, and the third third with the restriction endonuclease EcoRI; and

(iv) recombining the thirds after digestion in order to produce a population of linearized fragments of which about one-sixth of the population corresponds to the product of cleavage by each of the possible combinations of enzymes.]

A method for recognizing sequence identities and similarities between the sequence of a cDNA fragment corresponding to a mRNA molecule present in a sample and a database of sequences, comprising the steps of:

eluting a cDNA fragment corresponding to a mRNA molecule present in a sample;

amplifying the eluted cDNA fragment in a polymerase chain reaction to produce amplified cDNA fragment;

cloning the amplified cDNA fragment into a plasmid;

producing a DNA molecule corresponding to the cloned cDNA fragment;

sequencing the produced DNA molecule, thereby determining the sequence of the eluted cDNA fragment; and

comparing the sequence of the eluted cDNA fragment to the sequences in a database thereby recognizing sequence identities and similarities.

15. The method of claim [1] 14 wherein [the mRNA population has been enriched for polyadenylated mRNA species] the step of comparing the sequence of the eluted cDNA fragment to the sequences in a database is performed using a computer.

16. The method of claim [1] 15 [wherein the intensity of each band displayed after electrophoresis is about proportional to the abundance of the mRNA corresponding to the band in the original mixture] comprising the additional step of displaying the results of the comparison graphically.

17. [The method of claim 16 further comprising a step of determining the relative abundance of each mRNA in the original mixture from the intensity of the band corresponding to that mRNA after electrophoresis]

A method for recognizing sequence identities and similarities between the sequence of a cDNA fragment corresponding to a mRNA molecule present in a sample and a database of sequences, comprising the steps of :

eluting a cDNA fragment corresponding to a mRNA molecule present in a sample, where the cDNA fragment has a length determined by the position of a restriction endonuclease recognition site and a poly(A) tail of the mRNA molecule;

determining a partial sequence of the cDNA fragment by performing a polymerase chain reaction with a 5' PCR primer corresponding to the sequence of the restriction endonuclease recognition site and comparing the determined partial sequence of the eluted cDNA fragment and the length of the cDNA fragment to the sequences in a database thereby recognizing sequence identities and similarities.